

RESULT 1

ALDX_SPOSA

ID ALDX_SPOSA STANDARD; PRT; 322 AA.
AC P27800; Q12707;
DT 01-AUG-1992 (Rel. 23, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Aldehyde reductase I (EC 1.1.1.2) (Alcohol dehydrogenase [NADP+])
DE (ALR).
GN ARI.
OS Sporobolomyces salmonicolor.
OC Eukaryota; Fungi; Basidiomycota; Urediniomycetes;
OC Microbotryomycetidae; Sporidiobolales; Sporidiobolus.
OX NCBI_TaxID=5005;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 33-124; 132-153; 156-199 AND
RP 202-313, AND FUNCTION.
RC STRAIN=AKU 4429;
RX MEDLINE=96271678; PubMed=8779568;
RA Kita K., Matsuzaki K., Hashimoto T., Yanase H., Kato N.,
RA Chung M.C.-M., Kataoka M., Shimizu S.;
RT "Cloning of the aldehyde reductase gene from a red yeast,
RT Sporobolomyces salmonicolor, and characterization of the gene and its
RT product.";
RL Appl. Environ. Microbiol. 62:2303-2310(1996).
RN [2]
RP SEQUENCE OF 1-51, AND ENZYME REGULATION.
RC STRAIN=AKU 4429;
RX MEDLINE=92338224; PubMed=1633196;
RA Kataoka M., Sakai H., Morikawa T., Katoh M., Miyoshi T., Shimizu S.,
RA Yamada H.;
RT "Characterization of aldehyde reductase of Sporobolomyces
RT salmonicolor.";
RL Biochim. Biophys. Acta 1122:57-62(1992).
CC -!- FUNCTION: Catalyzes the asymmetric reduction of aliphatic and
CC aromatic aldehydes and ketones to an R-enantiomer. Reduces ethyl
CC 4-chloro-3-oxobutanoate to ethyl (R)-4-chloro-3-hydroxybutanoate.
CC -!- CATALYTIC ACTIVITY: An alcohol + NADP(+) = an aldehyde + NADPH.
CC -!- ENZYME REGULATION: Inhibited by quercetin, dicoumarol and some SH-
CC reagents.
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: Belongs to the aldo/keto reductase family.
CC -----
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CC -----
DR EMBL; U26463; AAB17362.1; -.
DR PIR; S78113; S78113.
DR HSSP; P15121; 2ACQ.
DR GO; GO:0005623; C:cell; IDA.
DR GO; GO:0008106; F:alcohol dehydrogenase (NADP) activity; IDA.
DR InterPro; IPR001395; Aldo/ket_red.

DR Pfam; PF00248; aldo_ket_red; 1.
 DR PRINTS; PR00069; ALDKETRDTASE.
 DR ProDom; PD000288; Aldo/ket_red; 1.
 DR PROSITE; PS00798; ALDOKETO_REDUCTASE_1; FALSE_NEG.
 DR PROSITE; PS00062; ALDOKETO_REDUCTASE_2; 1.
 DR PROSITE; PS00063; ALDOKETO_REDUCTASE_3; FALSE_NEG.
 KW Oxidoreductase; NADP.
 FT INIT_MET 0 0
 FT ACT_SITE 48 48 HYDROGEN-BOND DONOR (BY SIMILARITY).
 SQ SEQUENCE 322 AA; 35208 MW; 418A824DF5352DE1 CRC64;

Query Match 54.2%; Score 925; DB 1; Length 322;
 Best Local Similarity 57.4%; Pred. No. 4.4e-61;
 Matches 186; Conservative 38; Mismatches 84; Indels 16; Gaps 4;

Qy 9 LNDGNSIPALGYGTWQAEFGQVGEGVKLAVKAGYRHLDLAKVYQNQTEIGQALKELFDEG 68
 || | |: :||||| ||:||||:|:| :||||| || |:| |:| |
 Db 6 LNTGASLELVGYGTWQAAPGEVQGQGVKVAIETGYRHLDLAKVYSNQPEVGAAIK----EA 61
 Qy 69 VVKREDLFITSKLWNNRHAPEHVEPALDETLKELGLSYLDLYLIHWPVAFKFTTPDE--- 125
 ||||||||||||| | || |||||:||||| ||||||||| | |
 Db 62 GVKREDLFITSKLWNNSHRPEQVEPALDDTLKELGLELYLDLYLIHWPVAF----PPEGDI 117
 Qy 126 ---LLPADPTNKDLAYIDDSVKLSDTWKAVVALKKTGKTKSVGVSNFSTRLVDLVEEASG 182
 | | | :| | | ||||:| | ||| |:| ||| :||| :|||
 Db 118 TQNLFP--KANDKEVKLDLEVSLVDTWKAMVKLLDTGKVKAIGVSNFDAKMVDIAIIEATG 175
 Qy 183 ERPAVNQIEAHPLLQQDELVAHHKSKNIVITAYSPLGNVAGKPPLTENPGIVDAAKRLN 242
 |:|||| | || | ||:||||:|| | ||||||| | | | :|| | :|
 Db 176 VTPSVNQIERHPLLQPELIAHHKAKNIHITAYSPLGNNTVGAPLLVQHPEIKRIAENKNG 235
 Qy 243 HTPAAVLIAWGIQRGYSVLVKSVTSPRIKSNFEQITLSDEEFQRVTNLIKEYGESRNNVP 302
 ||| |||| | |:|: |||||| ||:|:| | : | : | :|
 Db 236 CTPAQVLIAWAIVGGHSSIPKSVTPSRIGENFKQVSLSQEDVDAVSKLGEKSGRRRYNIP 295
 Qy 303 FNYKPSWSIDVFGTQYEAKATHKI 326
 | | | |:| | : | : :
 Db 296 CTYSPKWDINVFGEDEKSCNAV 319

US-10-040-416-6

Query Match 99.4%; Score 1697; DB 13; Length 328;
Best Local Similarity 99.4%; Pred. No. 2.8e-156;
Matches 326; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MSYNKNIPLNDGNSIPALGYGTWQAEPGQVGEGVKLAVKAGYRHLDLAKVYQNQTEIGQA	60
Db	1	MSYNKNIPLNDGNSIPALGYGTWQAEPGQVGEGVKLAVKAGYRHLDLAKVYQNQTEIGQA	60
Qy	61	LKELFDEGVVKREDLFITSKLWNNRHAPEHVEPALDETLKELGLSYLDLYLIHWPVAFKF	120
Db	61	LKELFDEGVVKREDLFITSKLWNNRHAPEHVEPALDETLKELGLSYLDLYLIHWPVAFKF	120
Qy	121	TTPDELLPADPTNKDLAYIDDSVKLSDTWKAVVALKKTGKTKSVGVSNFSTRLVDLVEEA	180
		:	
Db	121	TTPDELLPADPTNKDLAYVDDSVKLSDTWKAVVALKKTGKTKSVGVSNFSTRLVDLVEEA	180
Qy	181	SGERPAVNQIEAHPLLQQDELVAHHKSKNIVITAYSPLGNNVAGKPPLTENPGIVDAAKR	240
Db	181	SGERPAVNQIEAHPLLQQDELVAHHKSKNIVITAYSPLGNNVAGKPPLTENPGIVDAAKR	240
Qy	241	LNHTPAAVLIAWGIQRGYSVLVKSVTSPRIKSNFEQITLSDEEFQRVTNLIKEYGESRNN	300
Db	241	LNHTPAAVLIAWGIQRGYSVLVKSVTSPRIKSNFEQITLSDEEFQRVTNLIKEYGESRNN	300
Qy	301	VPFNYKPSWSIDVFGTQYEA KATHKINA	328
Db	301	VPFNYKPSWSIDVFGTODEAKATHKINA	328

S78113

aldehyde reductase (NADPH) (EC 1.1.1.-) -fungus (Sporidiobolus salmonicolor)
N;Alternate names: NADPH-dependent aldehyde reductase
C;Species: Sporidiobolus salmonicolor, Sporobolomyces salmonicolor
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 11-Jun-1999
C;Accession: S78113; S23931
R;Kita, K.; Matsuzaki, K.; Hashimoto, T.; Yanase, H.; Kato, N.; Chung, M.C.;
Kataoka, M.; Shimizu, S.
submitted to the EMBL Data Library, May 1995
A;Description: Cloning of the aldehyde reductase gene from a red yeast,
Sporobolomyces salmonicolor, and characterization of the gene and its product.
A;Reference number: S78113
A;Accession: S78113
A;Molecule type: DNA
A;Residues: 1-323 <KIT>
A;Cross-references: EMBL:U26463; NID:g1142697; PIDN:AAB17362.1; PID:g1142698
A;Experimental source: strain AKU 4429
R;Kataoka, M.; Sakai, H.; Morikawa, T.; Katoh, M.; Miyoshi, T.; Shimizu, S.;
Yamada, H.
Biochim. Biophys. Acta 1122, 57-62, 1992
A;Title: Characterization of aldehyde reductase of Sporobolomyces salmonicolor.
A;Reference number: S23931; MUID:92338224; PMID:1633196
A;Accession: S23931
A;Molecule type: protein
A;Residues: 2-52 <KAT>
A;Experimental source: strain AKU 4429
C;Genetics:
A;Introns: 22/3; 47/3; 204/2; 242/2
C;Function:
A;Description: may be involved in detoxification of reactive carbonyl-containing
compounds; catalyzes the reduction of a wide range of aldehydes (but not e.g.
acetaldehyde) and ketones
A;Note: the authors use EC 1.1.1.2
C;Superfamily: aldehyde reductase
C;Keywords: NADP; oxidoreductase
F;2-323/Product: alcohol dehydrogenase (NADP+) #status experimental <MAT>

Query Match 54.2%; Score 925; DB 2; Length 323;
Best Local Similarity 57.4%; Pred. No. 2.8e-62;
Matches 186; Conservative 38; Mismatches 84; Indels 16; Gaps 4;

Qy	9 LNDGNSIPALGYGTWQAEPGQVGEGVKLAVKAGYRHLDLAKVYNQOTEIGQALKELFDEG	68
Db	7 LNTGASLELVGYGTWQAAPGEVQGQGVKVAIETGYRHLDLAKVYSNQPEVGAAIK----	EA 62
Qy	69 VVKREDLFITSKLWNNRHAPEHVEPALDETCLKELGLSYLDLYLIHWPVAFKFTTPDE---	125
Db	63 GVKREDLFITSKLWNNSHRPEQVEPALDDTLKELGLEYL DLYLIHWPVAF----	PPEGDI 118
Qy	126 ---LLPADPTNKDLAYIDDSVKLSDTWKAVVALKKTGKTKSVGSNFSSTRLV DLVEEASG	182
Db	119 TQNLP--KANDKEVKLDLEVSLVDTWKAMVKLLDTGKVKAIGVSNFDAKMVD AII EATG	176
Qy	183 ERPAVNQIEAHPLLQQDELVAHHKSKNIVITAYSPLGNNAVAGKPPLTENPGIVDAA KRLN	242
Db	177 VTSPVNOIERHP LLOPELIAHHKAKNIHITAYSPLGNNTV GAPLLVQHPEIKRIA EKNG	236

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Qy      243 HTPAAVLIAWGIQRGYSVLVKSVPTRISKNFEQITLSDEEFQRTNLIKEYGESRNNVP 302
      ||| |||| | | :||: ||||| ||:|:| | : | : | | :|
Db      237 CTPAQVLIAWAIVGGHSPKSVTPSRIGENFKQVSLSQEDVDAVSKLGEGSGRRRYNIP 296

Qy      303 FNYKPSWSIDVFGTQYEAKATHKI 326
      | | | |:| | : | : :
Db      297 CTYSPKWDINVFGEDEKSCKNAV 320

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